RAW SEQUENCE LISTING

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Application Serial Number: 10/540,063
Source: PCTTO
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RAW SEQUENCE LISTING DATE: 07/01/2005
PATENT APPLICATION: **US/10/540,063** TIME: 15:16:09

Input Set : **A:\Sequence Listing - 13311-00008-US.txt**
Output Set: **N:\CRF4\07012005\J540063.raw**

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      3 <110> APPLICANT: Geigenberger, Peter
      4       Langer, Anke
      5       Vigeolas, Helene
      6       Stitt Nigel, Marc
      7       van Dongen, Joost T.
      8       Udvardi, Michael
     10 <120> TITLE OF INVENTION: METHOD FOR ALTERING THE CONTENT OF RESERVE SUBSTANCES IN
PLANTS
     12 <130> FILE REFERENCE: 13311-00008-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/540,063
C--> 14 <141> CURRENT FILING DATE: 2005-06-22
     14 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014774
     15 <151> PRIOR FILING DATE: 2003-12-23
     17 <150> PRIOR APPLICATION NUMBER: DE 102 60 707.9
     18 <151> PRIOR FILING DATE: 2002-12-23
     20 <160> NUMBER OF SEQ ID NOS: 6
     22 <170> SOFTWARE: PatentIn version 3.3
     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 444
     27 <212> TYPE: DNA
     28 <213> ORGANISM: Lotus japonicus
     30 <220> FEATURE:
     31 <221> NAME/KEY: CDS
     32 <222> LOCATION: (1)..(444)
     34 <400> SEQUENCE: 1
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     37 1               5                  10                  15
     39 aca ttc aag aaa aac ctt cct acc aac agt gtt ttg ttc tac acc gtt    96
     40 Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val
     41             20                  25                  30
     43 ata ttg gag ata gca cca act gca aaa gac atg ttc tcc ttt cta aag   144
     44 Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys
     45         35                  40                  45
     47 gag tct ggg cct aag cat agt cct cag ctc cag gcc cat gct gaa aag   192
     48 Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
     49     50                  55                  60
     51 gtt ttt gca ctg act cgt gat gct gcc act caa ctc gta gca aaa gga   240
     52 Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
     53 65                  70                  75                  80
     55 gaa gtg aca ctt gca gat gcc agc tta ggt gct gtc cac gtt cag aaa   288
     56 Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
     57                 85                  90                  95
     59 gcc gtt act gat cct cat ttc gtg gtg gtt aaa gaa gcc ctg ctt caa   336
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60 Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
61             100                 105                 110
63 aca gta aag gaa gca gtt ggg gcg gac gaa tgg agt gat gac ttg agc   384
64 Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
65         115                 120                 125
67 acc gct tgg gaa gga gca tat gat gga cta gca act gca att aag aag   432
68 Thr Ala Trp Glu Gly Ala Tyr Asp Gly Leu Ala Thr Ala Ile Lys Lys
69     130                 135                 140
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72 Ala Met Gly
73 145
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 147
78 <212> TYPE: PRT
79 <213> ORGANISM: Lotus japonicus
81 <400> SEQUENCE: 2
82 Met Gly Phe Thr Ala Gln Gln Glu Ala Leu Val Gly Ser Ser Tyr Glu
83 1               5                  10                  15
85 Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val
86             20                  25                  30
88 Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys
89         35                  40                  45
91 Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
92     50                  55                  60
94 Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
95 65                  70                  75                  80
97 Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
98                 85                  90                  95
100 Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
101             100                 105                 110
103 Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
104         115                 120                 125
106 Thr Ala Trp Glu Gly Ala Tyr Asp Gly Leu Ala Thr Ala Ile Lys Lys
107     130                 135                 140
109 Ala Met Gly
110 145
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 483
116 <212> TYPE: DNA
117 <213> ORGANISM: Arabidopsis thaliana
119 <220> FEATURE:
120 <221> NAME/KEY: CDS
121 <222> LOCATION: (1)..(483)
123 <400> SEQUENCE: 3
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126 1               5                  10                  15
128 gta gtg aag tct tgg agt gtc atg aag aaa aac tca gct gaa tta ggt    96
129 Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly
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130              20                  25                  30
132 ctc aaa ctc ttc atc aag atc ttt gag att gca cca aca acg aag aag   144
133 Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
134          35                  40                  45
136 atg ttc tct ttc ttg aga gac tca cca att cct gct gag caa aat cca   192
137 Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
138      50                  55                  60
140 aag ctc aag cct cac gca atg tct gtt ttt gtc atg tgt tgt gaa tca   240
141 Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
142 65                  70                  75                  80
144 gca gta caa ctg agg aaa aca ggg aaa gtt acg gtg agg gag act act   288
145 Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
146                 85                  90                  95
148 ttg aag aga ctt gga gcc agc cat tct aaa tac ggt gtc gtt gac gaa   336
149 Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
150             100                 105                 110
152 cac ttt gag gtg gcc aag tat gca ttg ttg gag acg ata aag gag gca   384
153 His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
154          115                 120                 125
156 gtg ccg gag atg tgg tca ccg gag atg aag gtg gct tgg ggt cag gct   432
157 Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
158      130                 135                 140
160 tat gat cac ctt gtt gct gcc att aaa gct gaa atg aat ctt tcc aac   480
161 Tyr Asp His Leu Val Ala Ala Ile Lys Ala Glu Met Asn Leu Ser Asn
162 145                 150                 155                 160
164 taa                             483
167 <210> SEQ ID NO: 4
168 <211> LENGTH: 160
169 <212> TYPE: PRT
170 <213> ORGANISM: Arabidopsis thaliana
172 <400> SEQUENCE: 4
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174 1               5                   10                  15
176 Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly
177             20                  25                  30
179 Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
180          35                  40                  45
182 Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
183      50                  55                  60
185 Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
186 65                  70                  75                  80
188 Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
189                 85                  90                  95
191 Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
192             100                 105                 110
194 His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
195          115                 120                 125
197 Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
198      130                 135                 140
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201 145                 150                 155                 160
204 <210> SEQ ID NO: 5
205 <211> LENGTH: 477
206 <212> TYPE: DNA
207 <213> ORGANISM: Arabidopsis thaliana
209 <220> FEATURE:
210 <221> NAME/KEY: CDS
211 <222> LOCATION: (1)..(477)
213 <400> SEQUENCE: 5
214 atg gga gag att ggg ttt aca gag aag caa gaa gct ttg gtg aag gaa    48
215 Met Gly Glu Ile Gly Phe Thr Glu Lys Gln Glu Ala Leu Val Lys Glu
216 1               5                  10                  15
218 tcg tgg gag ata ctg aaa caa gac atc ccc aaa tac agc ctt cac ttc    96
219 Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe
220             20                  25                  30
222 ttc tca cag ata ctg gag ata gca cca gca gca aaa ggc ttg ttc tct   144
223 Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser
224         35                  40                  45
226 ttc cta aga gac tca gat gaa gtc cct cac aac aat cct aaa ctc aaa   192
227 Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
228     50                  55                  60
230 gct cat gct gtt aaa gtc ttc aag atg aca tgt gaa aca gct ata cag   240
231 Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
232 65                  70                  75                  80
234 ctg agg gag gaa gga aag gtg gta gtg gct gac aca acc ctc caa tat   288
235 Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
236                 85                  90                  95
238 tta ggc tca att cat ctc aaa agc ggc gtt att gac cct cac ttc gag   336
239 Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
240             100                 105                 110
242 gtg gtg aaa gaa gct ttg cta agg aca ttg aaa gag ggg ttg ggg gag   384
243 Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
244         115                 120                 125
246 aaa tac aat gaa gaa gtg gaa ggt gct tgg tct caa gct tat gat cac   432
247 Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
248     130                 135                 140
250 ttg gct tta gcc atc aag acc gag atg aaa caa gaa gag tca taa     477
251 Leu Ala Leu Ala Ile Lys Thr Glu Met Lys Gln Glu Glu Ser
252 145                 150                 155
255 <210> SEQ ID NO: 6
256 <211> LENGTH: 158
257 <212> TYPE: PRT
258 <213> ORGANISM: Arabidopsis thaliana
260 <400> SEQUENCE: 6
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262 1               5                  10                  15
264 Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe
265             20                  25                  30
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267 Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser
268         35                  40                  45
270 Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
271     50                  55                  60
273 Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
274 65                  70                  75                  80
276 Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
277                 85                  90                  95
279 Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
280             100                 105                 110
282 Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
283         115                 120                 125
285 Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
286     130                 135                 140
288 Leu Ala Leu Ala Ile Lys Thr Glu Met Lys Gln Glu Glu Ser
289 145                 150                 155
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VERIFICATION SUMMARY DATE: 07/01/2005
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Input Set : **A:\Sequence Listing - 13311-00008-US.txt**
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date